

## SEARCH REQUEST FORM

Requestor's Name: LORRAINE SPECTOR Serial Number: 09/185408  
Date: 7/13/00 Phone: 308-1793 Art Unit: 1647  
10B-11

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Point of Contact:  
Barb O'Bryen  
Technical Info. Specialist  
CM1 12C14 Tel: 308-4291

### STAFF USE ONLY

Date completed: <u>7-19-00</u>	Search Site	Vendors
Searcher: <u>LSB</u>	<input type="checkbox"/> STIC	<input checked="" type="checkbox"/> IG
Terminal time: <u>18 + 25 + 11 = 54</u>	<input type="checkbox"/> CM-1	<u>77</u> STN
Elapsed time: <u>11:30</u>	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: _____	<u>36</u> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<u>21</u> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: _____	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<u>67</u> Other
		<u>CEP</u>

! FINDPATTERNS on pir:\* allowing 0 mismatches

! 1 VCTYRDF(I,R,H,K)YRTV(E,R,H,K)PGCP(R,H,K)HVAPYFSPVA - *pattern searched*

Databases searched:

NBRF, Release 63.0, Released on 30Dec1999, Formatted on 7Mar2000

Total finds: 0

Total length: 58,629,743

Total sequences: 168,808

CPU time: 02:45.75

! FINDPATTERNS on swp:\* allowing 0 mismatches

! 1 VCTYRDF(I,R,H,K)YRTV(E,R,H,K)IPGCP(R,H,K)HVAPYFSYPVA

*continuation on next page*

Q15962 ck: 3504 len: 87

! Q15962 homo sapiens (human). thyrotropin be

1

VCTYRDF(I,R,H,K)YRTV(E,R,H,K)IPGCP(R,H,K)HVAPYFSYPVA

VCTYRDF(I)YRTV(E)IPGCP(H)HVAPYFSYPVA - *pattern matched*

VCTYRDFIYRTVEIPGCPHHVAPYFSYPVA

LSCKC

23: ALSOD

*matching portion of database seq*

Databases searched:

SWISS-PROT, Release 38.0, Released on 15Feb2000, Formatted on 16Feb2000

SPTREMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 1

Total length: 99,789,095

Total sequences: 309,735

CPU time: 04:30.74

*pattern searched*

```
!!AA SEQUENCE 1.0
ID Q15962 PRELIMINARY; PRT; 87 AA.
AC Q15962;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE THYROTROPIN BETA SUBUNIT (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93103017.
RA PEELE M.E., CARR F.E., BAKER J.R. JR., WARTOFKY L., BURMAN K.D.;
RT "TSH beta subunit gene expression in human lymphocytes.";
RL Am. J. Med. Sci. 305:1-7(1993).
DR EMBL; S51112; CAB30302.1; -.
DR HSP; P01233; IHRP_knot; 1.
DR PFAM; PF00007; 1
FT NON_TER 1
SQ SEQUENCE 87 AA; 9911 MW; B09DF839 CRC32;

Q15962 Length: 87 July 18, 2000 16:29 Type: P Check: 3504 ..

1 GYCMTRHNG KLFPLKIALS QDVCTYRDFI YRTVEIFGCP HHVAPYFSYP
51 VALSCRCGKC NTDYSDCTHE AVKTNCTKP QKSYLVG
```

! FINDPATTERNS on pir:\* allowing 0 mismatches

! 1 VCTYRDF(R,H,K)YRTV(E,R,H,K)IPGCF(L,R,H,K)HVAPYFSYPVA - *pattern searched*

Databases searched:

NBRF, Release 63.0, Released on 30Dec1999, Formatted on 7Mar2000

Total finds: 0

Total length: 58,629,743

Total sequences: 168,808

CPU time: 02:44.21

! FINDPATTERNS on swp:\* allowing 0 mismatches

! 1 VCTYRDF(R,H,K)YRTV(E,R,H,K)IPGCP(L,R,H,K)HVAPYFSYPVA - *pattern searched*

Databases searched:

SWISS-PROT, Release 38.0, Released on 15Feb2000, Formatted on 16Feb2000  
SPTREMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 0

Total length: 99,789,095

Total sequences: 309,735

CPU time: 04:34.90

! FINDPATTERNS on pir:\* allowing 0 mismatches

! 1 VCTYRDF(I,R,H,K)YRTV(R,H,K)IPGCP(L,R,H,K)HVAPYESYPVA - *pattern searched*

Databases searched:

NBRF, Release 63.0, Released on 30Dec1999, Formatted on 7Mar2000

Total finds: 0

Total length: 58,629,743

Total sequences: 168,808

CPU time: 02:43.05

! FINDPATTERNS on swp:\* allowing 0 mismatches

! 1 VCTYRDF(I,R,H,K)YRTV(R,H,K)IPGCP(L,R,H,K)HVAPYFSYPVA - *pattern searched*

Databases searched:

SWISS-PROT, Release 38.0, Released on 15Feb2000, Formatted on 16Feb2000  
SPREMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 0  
Total length: 99,789,095  
Total sequences: 309,735  
CPU time: 04:30.55



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> O <
O| IO IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "alpha-11" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
1 alpha-11 (AA) ID alpha-11 AA preliminary pattern
  followed by
2 apdvqdcpec
2 r or h or k
2 l
2 q or r or h or k
2 e or r or h or k
2 n
2 p or r or h or k
2 f or r or h or k
2 fs
2 q or r or h or k
2 pgapil

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries
Data bank : Issued_AA , all entries
Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:                               File Options:
Nucleic acid code matching      Exact      Indirect file      NO
Find non-matching hits only    NO         Sequence or key file  NO
Report key used                 Yes         List of hits         Yes
Note position of hit           Yes         Hit display          Yes
Display full annotations        Yes         Name and annotations Yes
Sequence context                10

Run mode                               Batch
Time to start comparison        now
Notify at end of run            NO

No hits found.

-- Run Parameters --

-- Search Statistics --

Times:                                CPU                                Total Elapsed
                                         00:21:19.04                       00:24:46.00

Number of sequences searched:          1068391
Number of sequence hits:              0
Number of separate matches:           0
Number of sequence hits saved:        0
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O| 10  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "alpha-13" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
alpha-13 (AA) ID alpha-13 AA preliminary pattern
1 followed by
2 apdvqdcpec
2 t or h or k
2 l or h or k
2 r or h or k
2 e or r or h or k
2 n
2 p or r or h or k
2 f or r or h or k
2 fs
2 q or r or h or k
2 pgapil
2

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries
Data bank : Issued_AA , all entries
Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact File Options:
Find non-matching hits only No Indirect file No
Report key used Yes Sequence or key file No
Note position of hit Yes List of hits Yes
Display full annotations Yes Hit display Yes
Sequence context 10 Name and annotations Yes

Run mode
Time to start comparison now Batch
Notify at end of run No

No hits found.

-- Run Parameters --

-- Search Statistics --

Times: CPU Total Elapsed
00:22:00.03 00:25:04.00

Number of sequences searched: 1068391
Number of sequence hits: 0
Number of separate matches: 0
Number of sequence hits saved: 0

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O| 10 Intelligenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "alpha-14" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
1 alpha-14 (AA) ID alpha-14 AA preliminary pattern
2 followed by
2 apdvqdcpec
2 t or h or k
2 l
2 q or r or h or k
2 r or h or k
2 n
2 p or r or h or k
2 f or r or h or k
2 fs
2 q or r or h or k
2 pgpil

Selected data banks and files:
Data bank : A-GenesSeq 35.2, all entries
Data bank : Issued_AA , all entries
Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact File Options:
Find non-matching hits only No Indirect file
Report key used Yes Sequence or key file
Note position of hit Yes List of hits
Display full annotations Yes Hit display
Sequence context 10 Name and annotations

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

No hits found.

-- Search Statistics --

Times:
CPU 00:20:36.07 Total Elapsed 00:34:24.00

Number of sequences searched: 1068391
Number of sequence hits: 0
Number of separate matches: 0
Number of sequence hits saved: 0

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OI IO IntelliGenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "alpha-16" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
alpha-16(AA) ID alpha-16 AA preliminary pattern
1 followed by
2 apdvqdcpec
2 t or h or k
2 l
2 q or r or h or k
2 e or r or h or k
2 n
2 r or h or k
2 f or r or h or k
2 fs
2 q or r or h or k
2 pgapil
2

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries
Data bank : Issued_AA, all entries.
Data bank : Pending_AA, all entries

-- Output Parameters --

Format Options:                               File Options:
Nucleic acid code matching      Exact      Indirect file      No
Find non-matching hits only    NO       Sequence or key file  NO
Report key used                 Yes      List of hits         Yes
Note position of hit           Yes      Hit display          Yes
Display full annotations        Yes      Name and annotations Yes
Sequence context                10

-- Run Parameters --

Run mode                          Batch
Time to start comparison         now
Notify at end of run             NO

No hits found.

-- Search Statistics --

Times:                            CPU              Total Elapsed
                                00:20:44.05      00:36:21.00

Number of sequences searched:      1068391
Number of sequence hits:           0
Number of separate matches:        0
Number of sequence hits saved:     0
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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "alpha-17" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
1 alpha-17 (AA) ID alpha-17 AA preliminary pattern
  followed by
2 apdvqdcpec
2 t or r or h or k
2 l
2 q or r or h or k
2 e or r or h or k
2 n
2 p or r or h or k
2 i or h or k
2 fs
2 q or r or h or k
2 pgapil

Selected data banks and files:
Data bank : A-GenesSeq 35.2, all entries
Data bank : Issued_AA , all entries
Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact Indirect file No
Find non-matching hits only Yes Sequence or key file No
Report key used Yes List of hits Yes
Note position of hit Yes Hit display Yes
Display full annotations Yes Name and annotations Yes
Sequence context 10

Run mode Batch
Time to start comparison now
Notify at end of run No

No hits found.

-- Run Parameters --

-- Search Statistics --

Times: CPU 00:20:47.04 Total Elapsed 00:23:12.00

Number of sequences searched: 1068391
Number of sequence hits: 0
Number of separate matches: 0
Number of sequence hits saved: 0
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OI IO IntelliGenetics
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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "alpha-20" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new key":
alpha-20(AA) ID alpha-20 AA Preliminary pattern
1 followed by
2 apdvqdcpec
2 t or r or h or k
2 l
2 q or r or h or k
2 e or r or h or k
2 n
2 p or r or h or k
2 f or r or h or k
2 fs
2 r or h or k
2 pgapil

Selected data banks and files:
Data bank : A-Geneseq 35.2, all entries
Data bank : Issued_AA , all entries
Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching. Exact NO
Find non-matching hits only NO Sequence or key file NO
Report key used Yes List of hits Yes
Note position of hit Yes Hit display Yes
Display full annotations Yes Name and annotations Yes
Sequence context 10

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run NO

No hits found.

-- Search Statistics --

Times: CPU Total Elapsed
00:20:57.12 00:35:56.00

Number of sequences searched: 1068391
Number of sequence hits: 0
Number of separate matches: 0
Number of sequence hits saved: 0

```

! FINDPATTERNS on pir:\* allowing 0 mismatches

! 1 APDVQDCPEC(T,R,K,H)L(O,R,H,K)(E,R,H,K)N(P,R,H,K)(F,R,H,K)FS(R,H,K)PGAPIL

*pattern searched*

Databases searched:

NBRF, Release 63.0, Released on 30Dec1999, Formatted on 7Mar2000

Total finds: 0

Total length: 58,629,743

Total sequences: 168,808

CPU time: 03:04.96

! FINDPATTERNS on swp:\* allowing 0 mismatches

! 1 APDVODCEC(T,R,K,H)L(Q,R,H,K)(E,R,H,K)N(P,R,H,K)(F,R,H,K)FS(R,H,K)PGAPIL - *pattern searched*

Databases searched:

SWISS-PROT, Release 38.0, Released on 15Feb2000, Formatted on 16Feb2000  
SPRMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 0  
Total length: 99,789,095  
Total sequences: 309,735  
CPU time: 05:07.96